

AMENDMENTS TO THE CLAIMS

1. (Currently Amended) A method for the analysis of a target sequence in a first sample, said method comprising:
 - a--contacting the first sample with a mixture comprising:
~~[[A]] mixture of two-probes (probe A and probe B}, wherein Probe A and Probe B are PNA probes, and wherein:~~
 - i) Probe A is ~~eomprised of a nucleotide sequence~~, directed to a region of the target sequence and is labeled with a fluorophore at the end which, upon hybridization is closest to the adjacent target region for Probe B; ~~and~~
 - ii) Probe B is ~~eomprised of a nucleotide sequence, which~~ cohybridizes to a region of the target sequence adjacent to the target region of Probe A and is labeled with a quencher which, upon hybridization is closest to the adjacent target region for Probe A, ~~and~~
 - b--measuring fluorescence following cohybridization of Probe A and Probe B to the target sequence, under suitable hybridization conditions, wherein the presence or amount of target sequence present in the first sample can be negatively correlated with the fluorescence of the fluorophore on Probe A.
2. (Original) The method of claim 1, wherein the fluorescence is measurably different than a control.
3. (Original) The method of claim 2, wherein the control is a positive control, a negative control, a no target control or a second sample.
4. (Original) The method of claim 3, wherein the fluorescence is taken to be indicative of an increase in target concentration, a structural difference between sample and control target sequences or a change in the state of the target sequence.
5. (Original) The method of claim 4, wherein the structural difference between sample and control target sequences is at least one of a nucleobase insertion, nucleobase deletion, genetic polymorphism, splice variation, amplification or mutation.

6. (Original) The method of claim 4, wherein the change in target state is due to at least one of degradation, methylation, folding, hybridization, or association of the target sequence with protein.

7. (Original) The method of claim 1, wherein the target sequence for Probe A and Probe B comprise at least one nucleobase differing from non-target sequences.

8. (Original) The method of claim 7, wherein the method is used to detect target sequence in a closed tube (homogeneous) assay.

9. (Original) The method of claim 7, wherein the method is used to detect a nucleic acid comprising a target sequence wherein said nucleic acid has been synthesized or amplified in a reaction occurring in the closed tube (homogeneous) assay.

10. (Original) The method of claim 9, wherein preferred nucleic acid synthesis or nucleic acid amplification reactions are selected from the group consisting of: Polymerase Chain Reaction (PCR), Ligase Chain Reaction (LCR), Strand Displacement Amplification (SDA), Transcription-Mediated Amplification (TMA), Rolling Circle Amplification (RCA) and Q beta replicase.

11. (Original) The method of claim 10, wherein the PCR reaction is an asymmetric PCR reaction.

12. (Original) The method of claim 1, wherein the method further comprises contacting the sample with at least one blocking probe.

13. (Original) The method of claim 12, wherein the method further comprises hybridizing the blocking probe to non-target sequences.

14. (Cancelled)

15. (Original) The method of claim 1, wherein the method is used to detect, identify, or quantitate the presence or amount of one or more species or types of a microorganism in the sample.

16. (Original) The method of claim 1, wherein the method is used to determine the effect of antimicrobial agents on the growth of one or more microorganisms in the sample.

17. (Original) The method of claim 1, wherein the method is used to determine the presence or amount of a taxonomic group of microorganisms in the sample.

18. (Original) The method of claim 1, wherein the method is used to diagnose a condition of medical interest.

19. (Original) The method of claim 1, wherein the target sequence is immobilized to a surface.

20. (Original) The method of claim 1, wherein Probe A is immobilized to a surface.

21. (Original) The method of claim 1, wherein Probe A is one component of an array.

22.-25. (Cancelled)

26. (Original) The method of claim 12, wherein the blocking probe is PNA or LNA.

27. (Original) The method of claim 12, wherein the blocking probe is a nucleic acid comprising LNA.

28. (Original) The method of claim 1, wherein at least one of the probes is a linear PNA beacon.

29. (Original) The method of claim 1, wherein the sample comprises a target sequence which is indicative for a genetically based disease or is indicative for a predisposition to a genetically based disease

30. (Original) The method of claim 1, wherein the target sequence is associated with a disease selected from the group consisting of 5-Thalassemia, sickle cell anemia, Factor-V Leiden, cystic fibrosis and cancer related targets such as p53, p10, BRC-1 and BRC-2.

31. (Currently Amended) The method of claim 1, wherein the target sequence is detected in a forensic technique such as prenatal screening, paternity testing, identity confirmation or crime investigation.

32.-41. (Cancelled)

42. (New) The method of claim 1, wherein the target sequence is rRNA.

43. (New) The method of claim 1, wherein the amount of target sequence detects, identifies or qualifies the presence or amount of an organism or virus in the sample.